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> O <
O | O   IntelliGenetics
> O <
```

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file seq12-seq24.res made by jdelaval on Tue 26 Apr 105 5:56:19-PST.

Query sequence being compared:US-10-072-622-12 (1-199)
Number of sequences searched:                    1
Number of scores above cutoff:                   1

Results of the initial comparison of US-10-072-622-12 (1-199) with:
File : 6521749.pep



```
SCORE  0     13    27    40    54    67    81    94   108   121
STDEV  |-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
100-
  |
 N  |
50- |
  U |
  M |
  B |
  E |
  R |
    |
100-|
  O |
  F |
    |
 10-|
  O |
  F |
  S |
  5-|
  S |
  C |
  O |
  R |
  E |
  S |
  0-|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----*|
```

PARAMETERS

| | Unitary | K-tuple | 1 | 2 |
|---|---|---|---|---|
| Similarity matrix | 1 | Joining penalty | 20 | |
| Mismatch penalty | 1.00 | Window size | 32 | |
| Gap penalty | 1.00 | | | |
| Gap size penalty | 0.05 | | | |
| Cutoff score | 0 | | | |
| Randomization group | 0 | | | |

SEARCH STATISTICS

| | Mean | Median | Standard Deviation |
|---|---|---|---|
| Scores: | 121 | 0 | 0.00 |

| | | CPU | Total Elapsed |
|---|---|---|---|
| Times: | | 00:00:00.00 | 00:00:00.00 |

| Number of residues: | 379 |
|---|---|
| Number of sequences searched: | 1 |
| Number of scores above cutoff: | 1 |

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

---

| Sequence Name | Description | Length | Init. Score | Opt. Score | Sig. | Frame |
|---|---|---|---|---|---|---|
| 1. US-09-667-135-24 Sequence 24, Application US/09667135 | | 379 | 121 | 132 | 0.00 | 0 |

```
1. US-10-072-622-12 (1-199)
   US-09-667-135-24 Sequence 24, Application US/09667135

Sequence 24, Application US/09667135
Patent No. 6521749
GENERAL INFORMATION:
APPLICANT: Vincent Ling
APPLICANT: Kyriaki Dunussi-Joannopoulos
TITLE OF INVENTION: NOVEL GL50 MOLECULES AND USES THEREFOR
FILE REFERENCE: GNN-007
CURRENT APPLICATION NUMBER: US/09/667,135
CURRENT FILING DATE: 2000-09-21
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 24
LENGTH: 379
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION:.hiCOS-mIgG2am amino acid sequence
```

| Initial Score | = | 121 | Optimized Score | = | 132 | Significance | = | 0.00 |
|---|---|---|---|---|---|---|---|---|
| Residue Identity | = | 66% | Matches | = | 137 | Mismatches | = | 55 |
| Gaps | = | 15 | Conservative Substitutions | = | 0 | | | |

```
            X         10         20         30         40         50         60
           MKSGLMYFFLFCLRIKVL------TGEINGSANYEMFIFHNGGVQILCKYPDIVQQFKMQLLKGGQILCDLTK
           |||||||||||||||||      |||||||||||||||||||||||||||||||||||||||||||||||||
           MGVLLTQRTLLSLVLALLFPSMASMEINGSANYEMFIFHNGGVQILCKYPDIVQQFKMQLLKGGQILCDLTK
            X         10         20         30         40         50         60         70

          70         80         90        100        110        120        130
          TKGSGNTVSIKSLKFCHSQLSNNSVSFFLTNLDHSHANYFCNLSIFDPPPFKVTLTGGYLHIYESQLCCQL
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
          TKGSGNTVSIKSLKFCHSQLSNNSVSFFLTNLDHSHANYFCNLSIFDPPPFKVTLTGGYLHIYESQLCCQL
          80         90        100        110        120        130        140

         140        150        160        170        180        190          X
         KFWLPIGCAAFVVVCILGC-ILICWLTKKKYSSSSV--HDPNGEYMPMRAVNTAKSRLTDVTL
         |||||||||||||||||||   ||||||||||         ||               ||||
         KF-EPRG------PTIKPCPPCKCPAPNLRGGPSVPIFPPKIKDVLMISLSPIVTCVVVDVSEDDPDVQISW
         150        160        170        180        190        200

         FVNNVEVHTAQTQTHREDYNSTLRVVSALPIQHQDDMSGKAFACAVNNKDLPAPIERTISKPKGSVRAPQVY
         210        220        230        240        250        260        270        280

         VLPPPEEMIKKQVTLTCMVTDFMPEDIYVEWTNNGKTELNYKNTEPVLDSDGSYFMYSKLRVEKKNWVERN
         290        300        310        320        330        340        350

         SYSCSVVHEGLHNHHTTKSFSRTPGK
         360        370
```